embodiment of the present invention refolding is performed in the simultaneous presence of cysteine and cystine in the refolding buffer. By adjusting the amounts and mutual ratio of cysteine and cystine, one can produce the desired mix of VEGF dimers. The latter embodiment is specifically illustrated in the Examples below. In a preferred embodiment, free cysteine used in the refolding step is added in molar excess from about 4-fold to about 40-fold over the cysteines present in the VEGF polypeptide. More preferably, the free cysteine is used in from about 4-fold to about 20-fold, even more preferably from about 4-fold to about 10-fold, most preferably about 10-fold molar excess over the cysteines present in the VEGF polypeptide. The cysteine to cystine molar ratio generally is between about 2:1 and 20:1, preferably between about 2:1 and 10:1, more preferably between about 2:1 and 5:1, most preferably about 4:1 and 5:1.

IN THE CLAIMS:

Please cancel claims 4, 12, 22, 23, 24, 26-34 without prejudice.

Please amend claims 1, 2, 13, 14, 15, and 17 as follows:

1. (Amended) A vascular endothelial growth factor (VEGF) variant dimer consisting of a first monomer and a second monomer, comprising an amino acid sequence having at least about 90% sequence identity with amino acids 11 to 116 of SEQ ID NO: 1, retaining a cysteine (Cys) at or corresponding to position 116 of SEQ ID NO: 1 (Cys-116), wherein the Cys of each monomer is disulfide-bonded to an additional extraneous Cys, and wherein at least one monomer possesses a glycosylation site at or corresponding to positions 75-77 of SEQ ID NO: 1 that has been eliminated.

2. (Amended) The VEGF dimer of claim 1 wherein the Cys residue in at least one of said first monomer or second monomers, or both, is disulfide-bonded to a peptide of 2-5 amino acids.

13. (Amended) The VEGF dimer of claim 1 wherein said first and second monomers are unglycosylated.

14. (Amended) A composition comprising a vascular endothelial growth factor (VEGF) dimer consisting of a first monomer and a second monomer, each monomer comprising an amino acid sequence having at least about 90% sequence identity with amino acids 11 to 116 of SEQ ID NO: 1, wherein at least one monomer possesses a glycosylation site at or corresponding to positions 75-77 of SEQ ID NO: 1 that has been eliminated, and retaining a